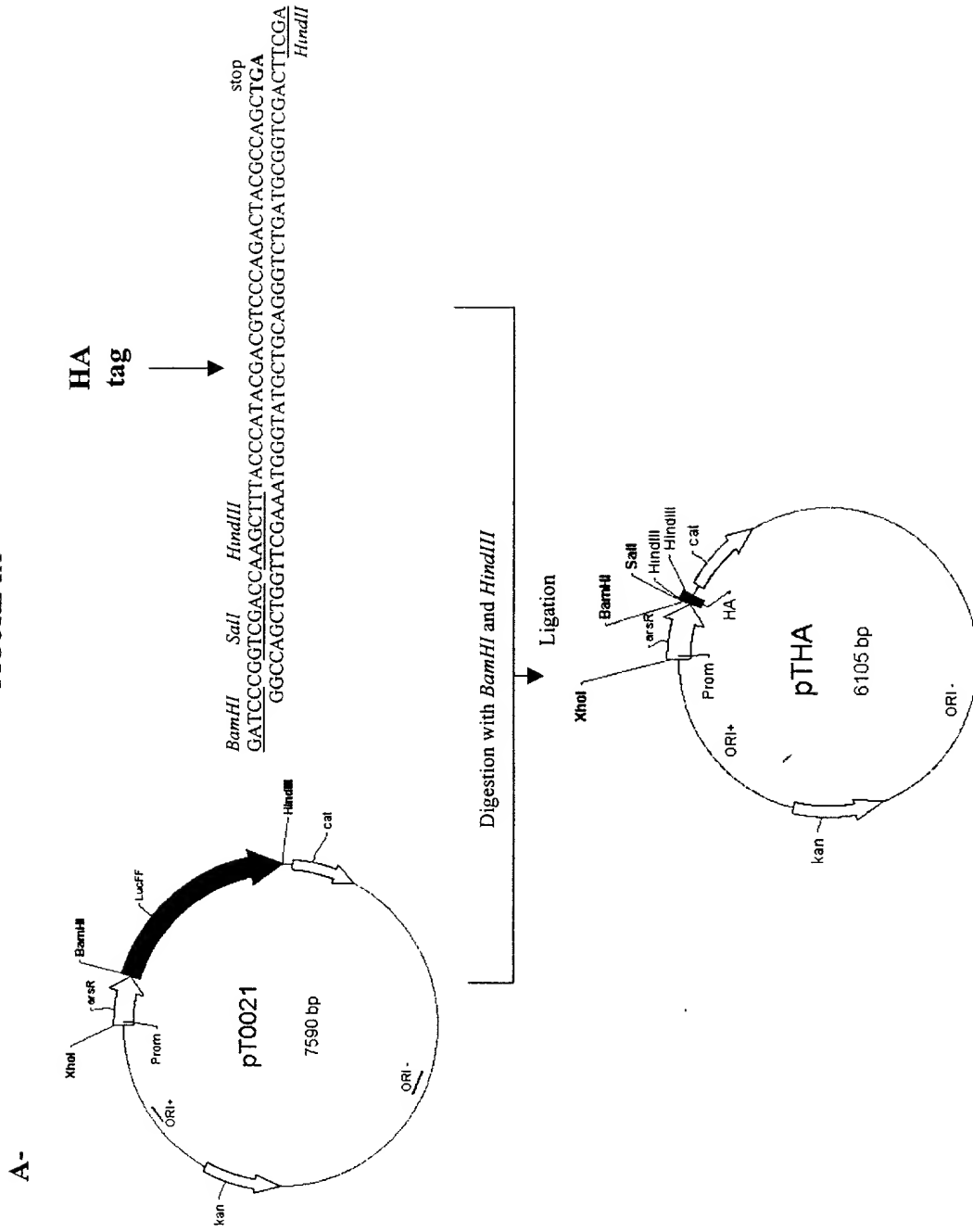


FIGURE 1A



B-

FIGURE 1B

PCR of pT0021 with XhoF and BamHNR

XhoF-5'-AATTCTCGAGTAAAATAACAT-3  
XhoI

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR  
Stop of  
arsR RBS BamHI

Digestion with XhoI and BamHI

Ligation

PCR of pT0021 with LucFFB and LucFFH

LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG  
BamHI Start Original BamHI  
of LucFF was modified

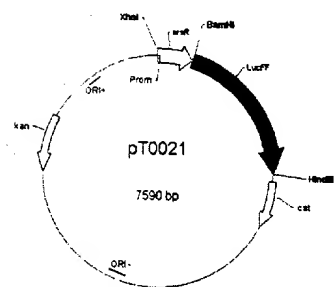
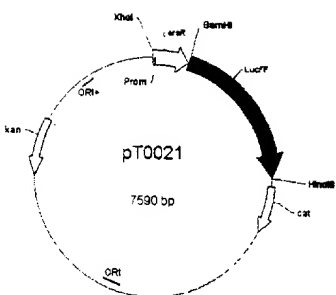
GAAAGTCCAAATTGTAAGCTTGGG-LucFFH  
Stop of HindIII  
LucFF

Digestion with BamHI and HindIII

Ligation

- Modified in the vicinity of BamHI
- Cloning site for ORFs: BamHI and HindIII
- No additional codons in the induced protein

Prom arsR LucFF  
CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT  
XhoI RBS BamHI HindIII



Modified between stop  
of arsR to BamHI

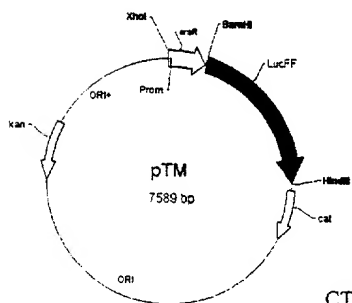
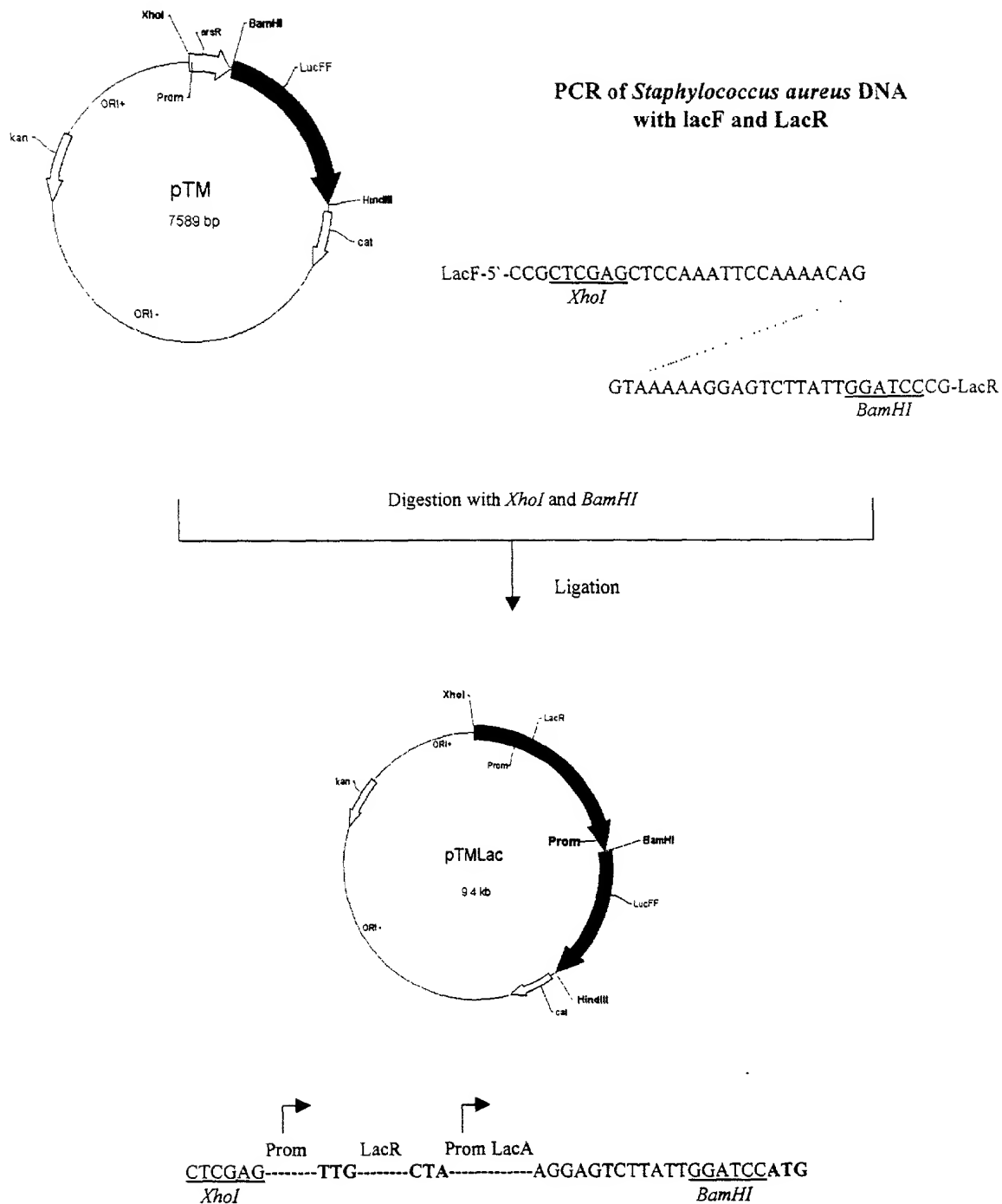


FIGURE 1C

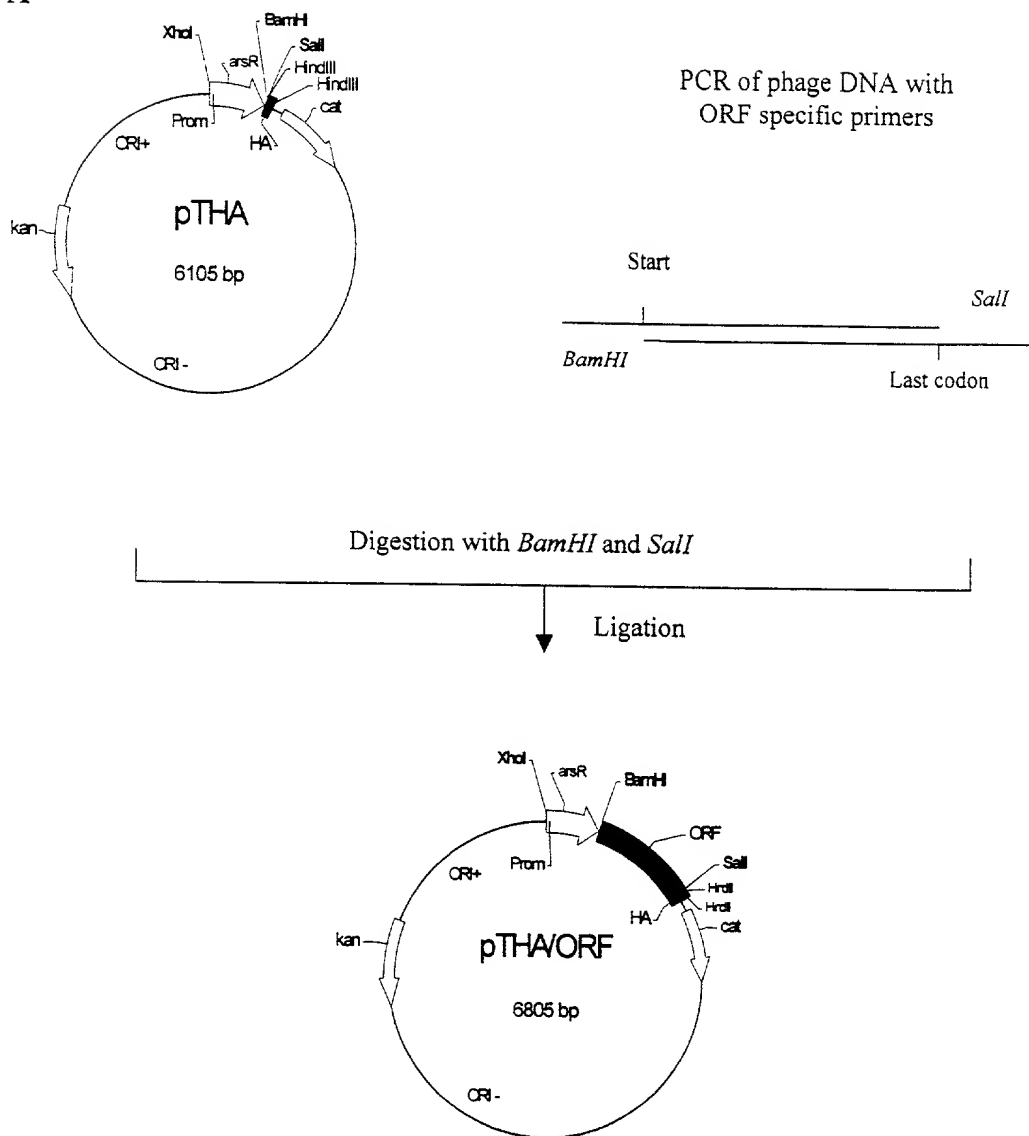
C-



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FIGURE 2A

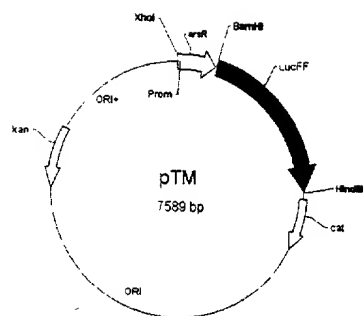
A-



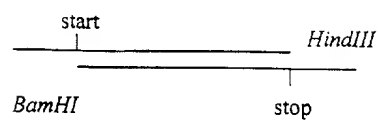
0972392-031001

FIGURE 2B

B-

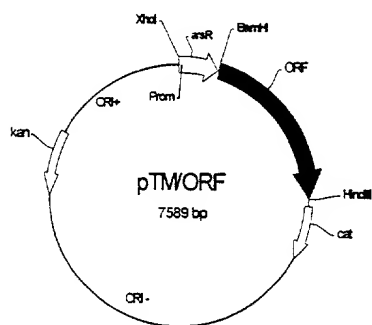


PCR of phage DNA with  
ORF specific primers



Digestion with *Bam*HI and *Hind*III

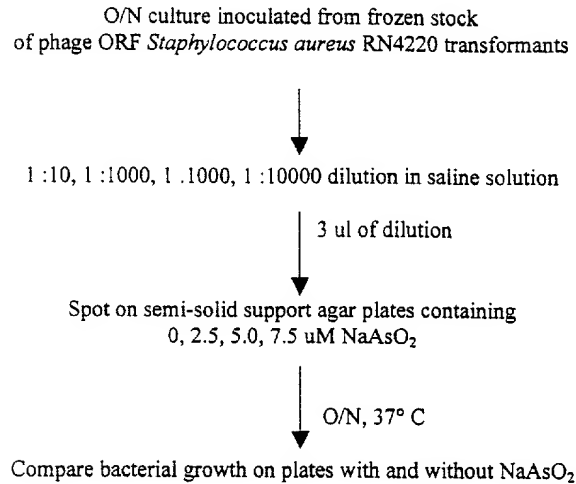
Ligation



09727392-031001

FIGURE 3

A) Functional assay on semi-solid support medium



B) Functional assay in liquid medium

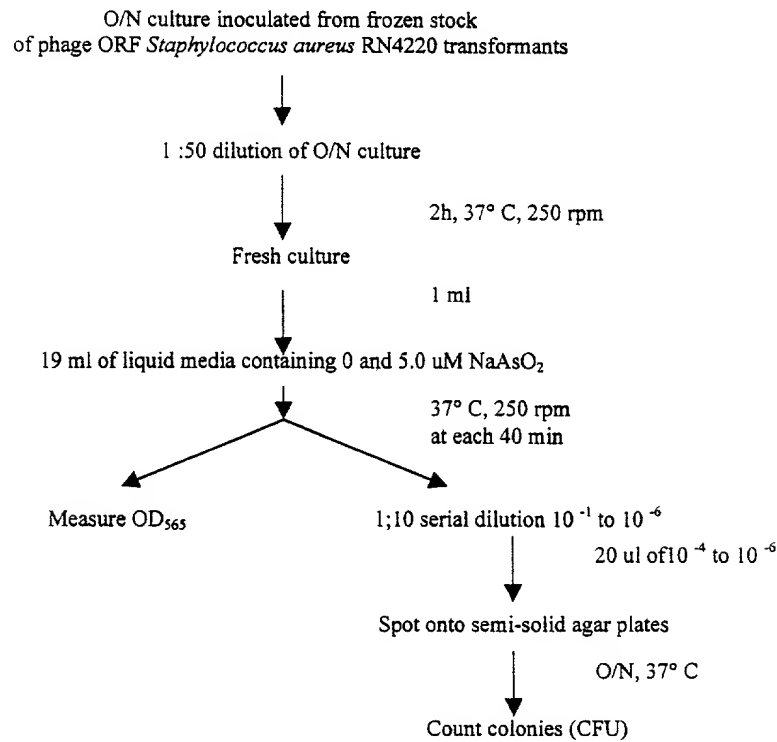


FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

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A-

FIGURE 5A

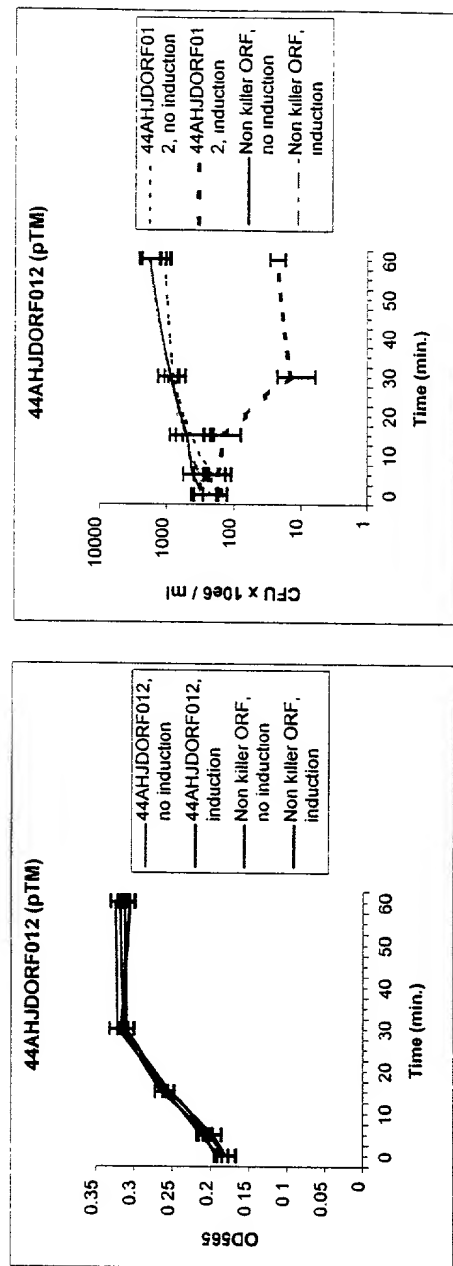
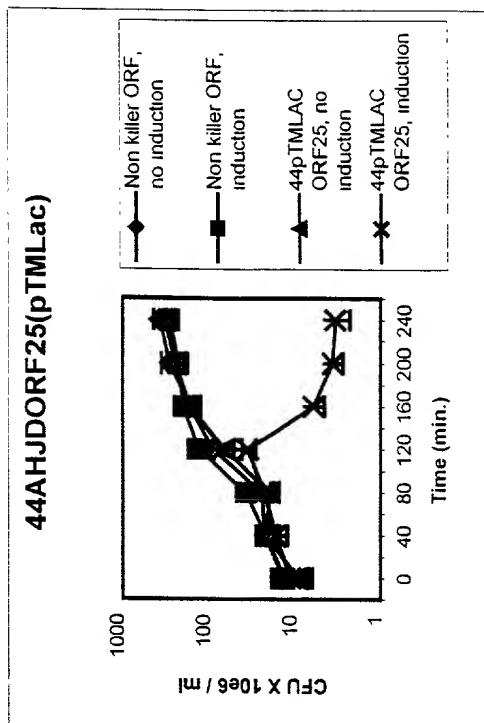
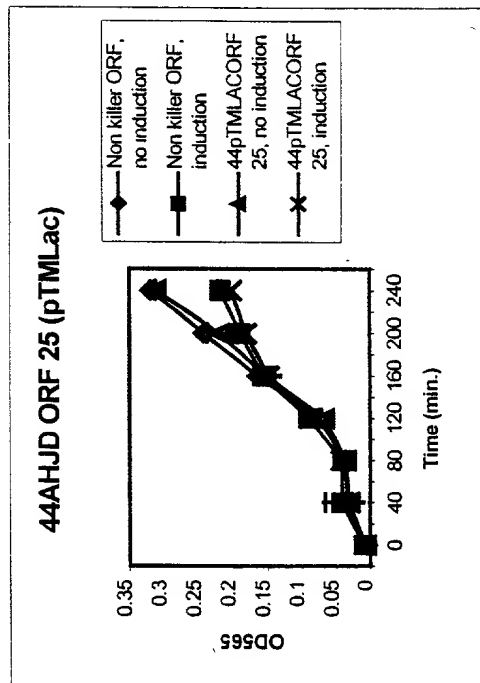
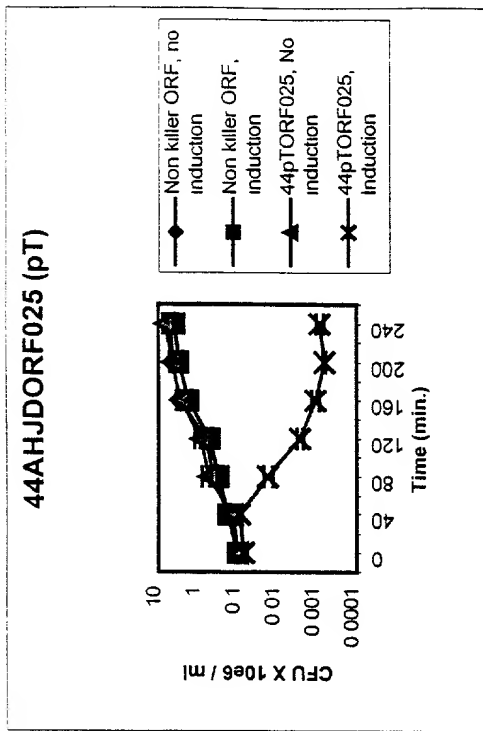
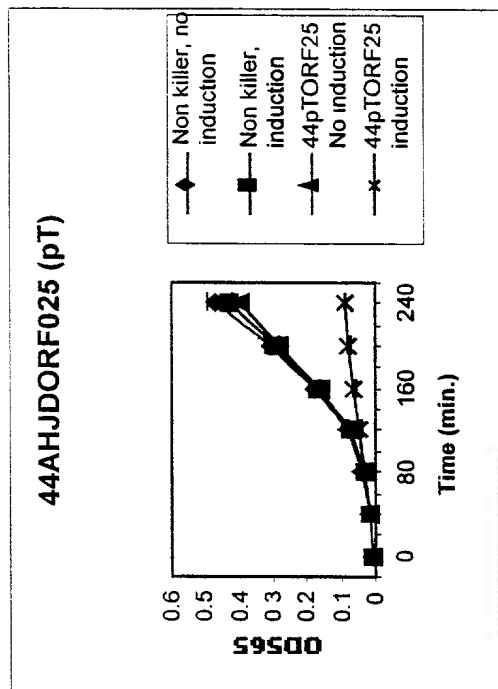
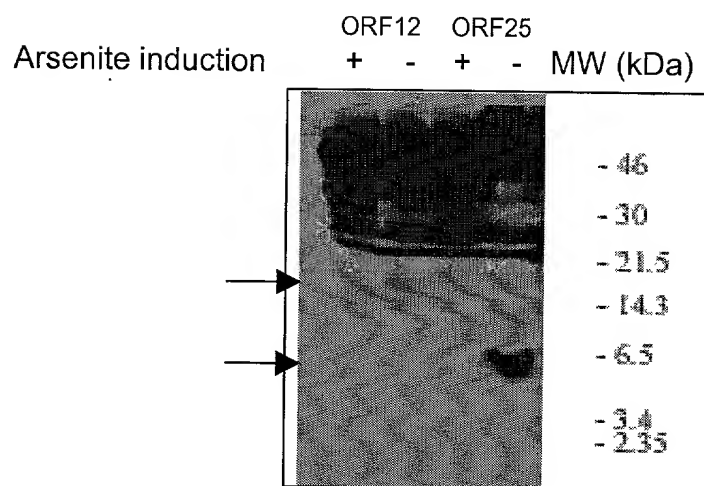


Fig  
.5B

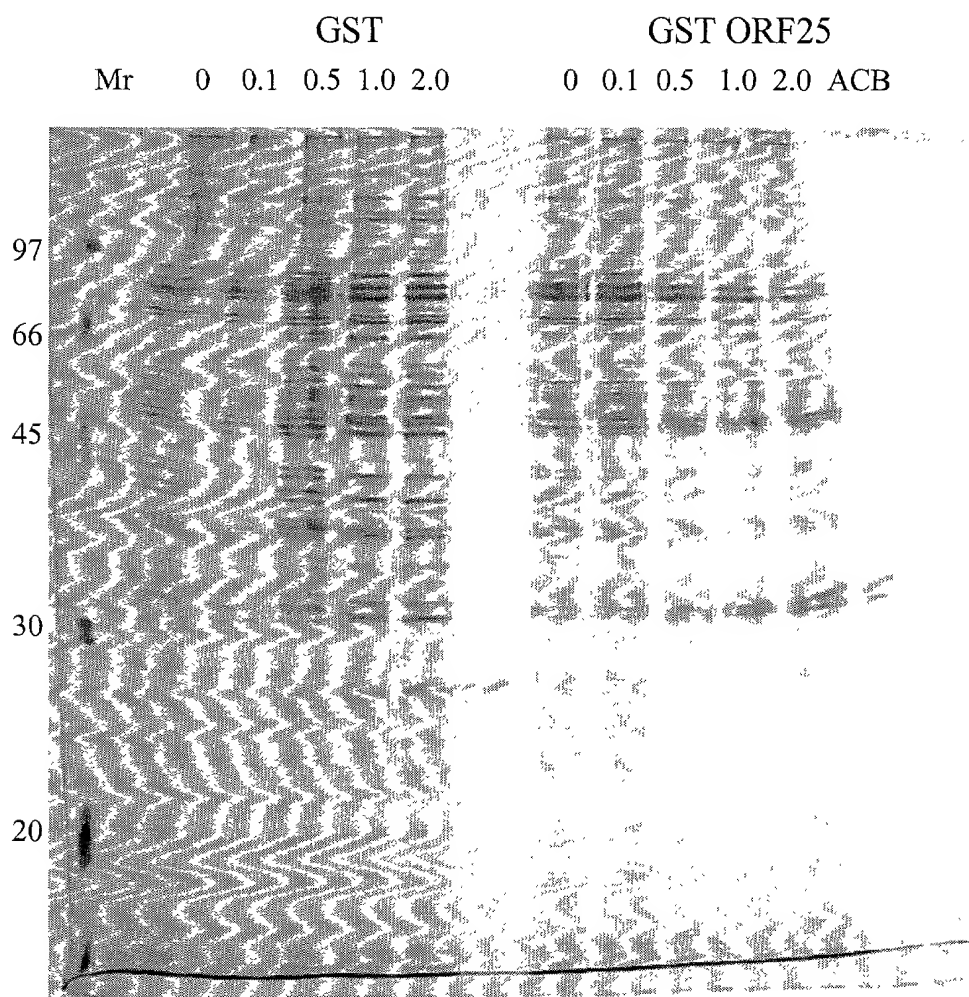


**FIGURE 6**



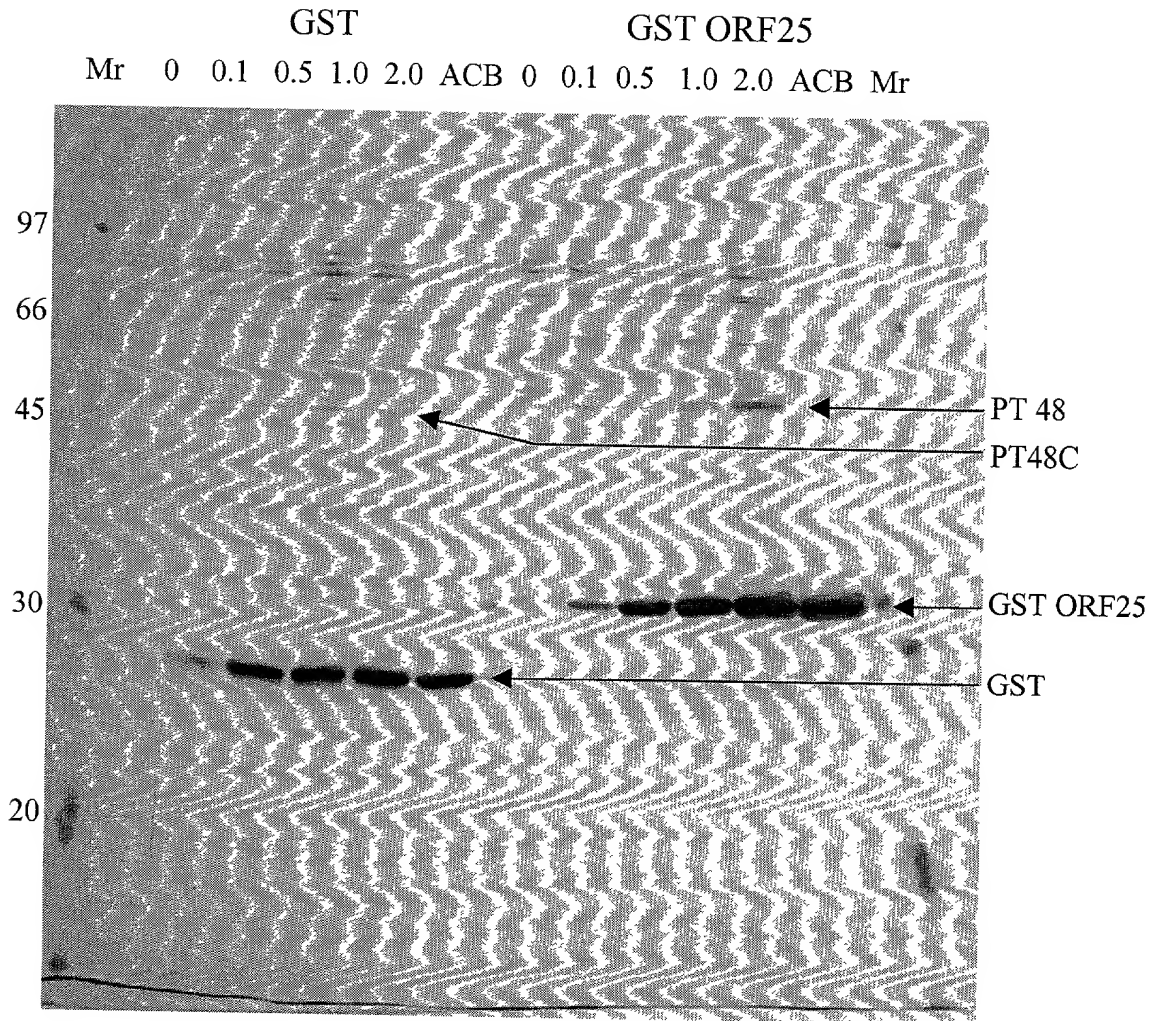
007227892-031001

FIGURE 7A



0022893.03401

FIGURE 7B



09727892-081001

[illegible][illegible]

**A**

**B**

**C**

**D**

**E**

**F**

**G**

**H**

**I**

**J**

**K**

**L**

**M**

**N**

**O**

**P**

**Q**

**R**

**S**

**T**

**U**

**V**

**W**

**X**

**Y**

**Z**

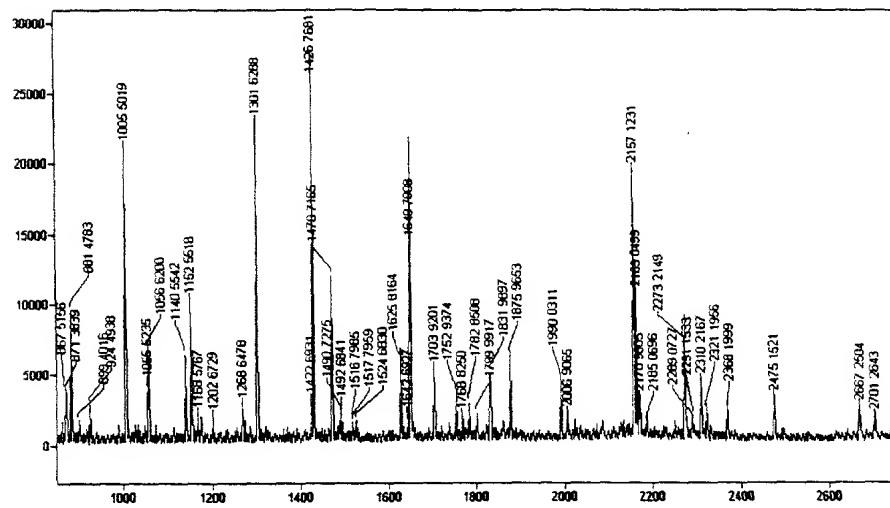
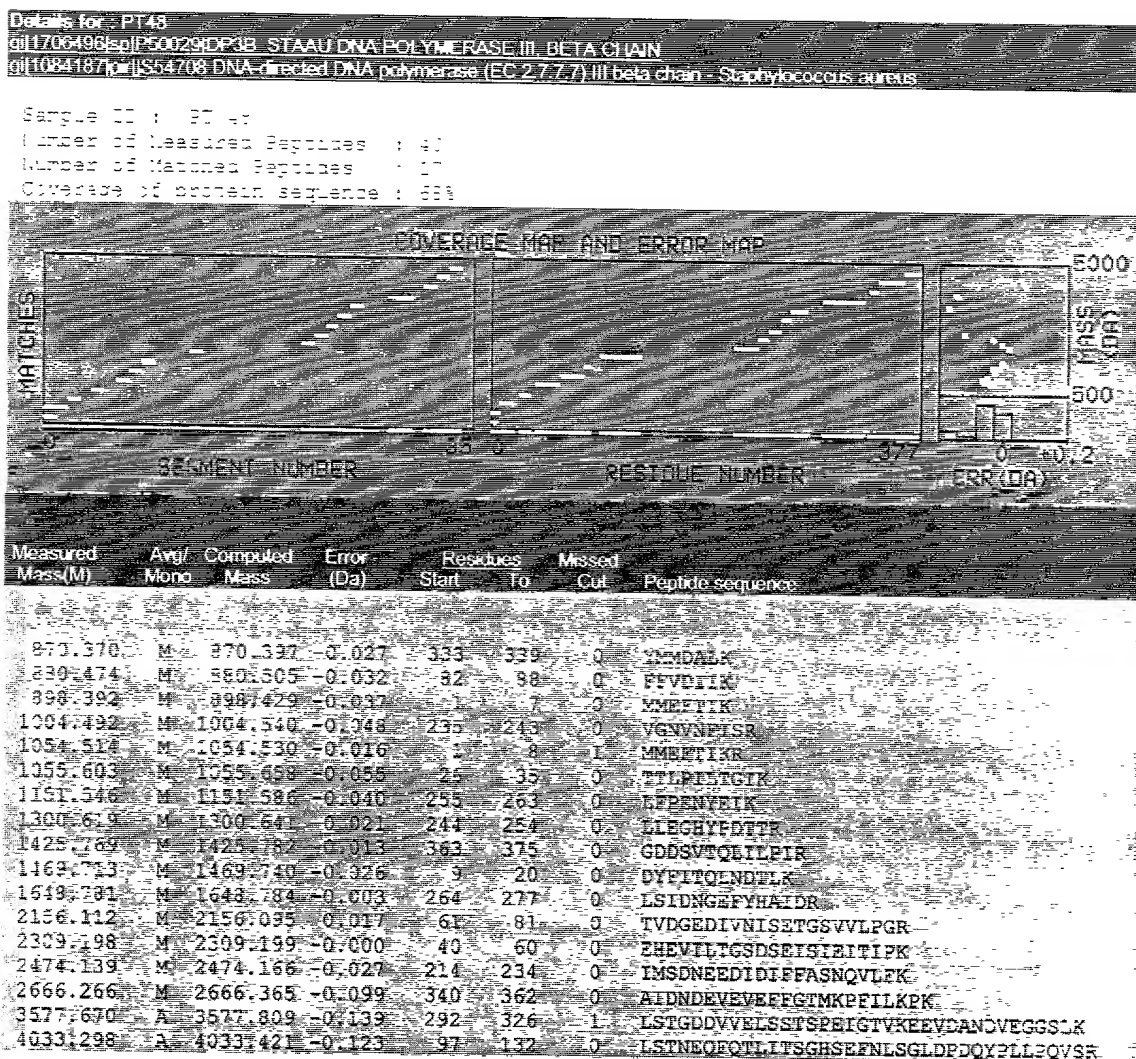


FIGURE 9

Identification of PT-8 as DNA-directed DNA polymerase III beta.



097227892-081001

## FIGURE 10

### SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCATAATTAAGAGATTATTTTATTACACAATTAATGACACATTAAAA  
GCTATTTACCAAGAACAACATTACCTATATTAAGTGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAAGTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATTTTTCAGAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCAGACATTAATTACATCAGGTCATTCTGAATTTAATTAAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC  
CCAGTACTAAGTGGTGTGAAGTGGCTTATACAAGAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAATAAAATTTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTATTTAAAGTTGGAAATGTGAACCTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCTGAAAACAT  
GAAATTAATAAGTATAGACAATGGGGAGTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATAAGTACAGGTGATGACGTTGTTGAA  
TTGTCTTCTACATCACCAGAAATTTGTTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT  
GAAGGTGGTAGCTGAAAATTTTCACTCAACTCTAAATATATGATGGATGCTTTAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCCTTCGGTACAATGAAACCATTATTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

### SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
*Staphylococcus aureus*

MMEFTIKRDYFITQLNDTLKAISPRITLPIITGKIDAKEHEVILTGSSEISIEITIPKTVGDGDIVNI  
SETGSVVLPGREFVDIIKKLPGKDVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLQVSRDDAIQLSV  
KVLKNVIAQTNEAVSTSETRPVLTGVNWLIIQENELICTATDSHRLAVRKLQLEDVSENKNVVIIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKGVNVNFISSLLEGHYPDTTTLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEVDANDVEGGSLLKISFNSKYMDALKAIIDNDEVEVEF  
FGTMKPFILPKGDDSVTQLILPIRTY